

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _____

Source: _____

Date Processed by STIC: _____

10/699,874A
JFW/6
02/22/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/699,874 A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|--|--|
| 1 | _____ Wrapped Nucleics
Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | _____ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | _____ Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead. |
| 4 | _____ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | _____ Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | _____ PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | _____ Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | _____ Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional , please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | _____ Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents. |
| 10 | _____ Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 1:1 below) |
| 11 | _____ Use of <220> | <u>Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules</u> |
| 12 | _____ PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | _____ Misuse of n/Xaa | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u> |



IFW16

RAW SEQUENCE LISTING

DATE: 02/22/2007

PATENT APPLICATION: US/10/699,874A

TIME: 13:48:32

Input Set : E:\AM100788_Seq_list_total.txt

Output Set: N:\CRF4\02222007\J699874A.raw

4 <110> APPLICANT: WYETH HOLDING CORPORATION.; KUNZ, ARTHUR ET AL.
 6 <120> TITLE OF INVENTION: CALICHEAMICIN DERIVATIVE-CARRIER CONJUGATES
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/699,874A
 C--> 9 <141> CURRENT FILING DATE: 2003-11-03
 W--> 0 <130> FILE REFERENCE:
 9 <160> NUMBER OF SEQ ID NOS: 61
 11 <170> SOFTWARE: SeqWin99, version 1.02

ERRORS SEQUENCES

1322 <210> SEQ ID NO: 61
 1323 <211> LENGTH: 23
 1324 <212> TYPE: PRT
 1325 <213> ORGANISM: Artificial
 1327 <220> FEATURE:
 1328 <223> OTHER INFORMATION: gL2 graft
 1330 <400> SEQUENCE: 61
 1332 Ser Arg Gly Asp Val Val Thr Gln Ser Pro Ser Ser Leu Ser Ala
 1333 1 5 10 15
 1336 Ser Val Gly Asp Arg Val Thr
 1337 20
 1340 AM100788
 E--> 1345 23
 1348 AM100788
 E--> 1350 1

Does Not Comply
 Corrected Diskette Needed

(pg-1)

Insufficient Explanation
 Pls give
 the source
 of genetic
 material.
 See Item
 11 on Error
 Summary
 Sheet.

Pls delete

FYI:- Pls Check the
 Entire Sequences
 for Subsequent
 Responses

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/22/2007
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:52,53,54,55,56,57,58,59,60,61

VERIFICATION SUMMARY

DATE: 02/22/2007

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TIME: 13:48:33

Input Set : E:\AM100788_Seq_list_total.txt

Output Set: N:\CRF4\02222007\J699874A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:22 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:37 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:55 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:70 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:86 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:101 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:116 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:152 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:188 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:203 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:218 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:233 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:248 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:266 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:267 M:283 W: Missing Blank Line separator, <400> field identifier
L:280 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:298 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:316 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:343 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:394 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:430 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:458 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:473 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:509 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:545 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:25
L:581 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:617 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:653 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:710 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:737 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:839 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:888 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:903 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:918 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:933 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:948 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:963 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:978 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:992 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:1006 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:1021 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:1036 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42
L:1051 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:1066 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44

VERIFICATION SUMMARY

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L:1081 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:1096 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
L:1110 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:1124 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
L:1143 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:1345 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61
L:1350 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:61